

SEQUENCE LISTING

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DOS SANTOS, JEAN-PHILIPPE
MEJEAN, VINCENT

<120> NUCLEOTIDE SEQUENCES DERIVED FROM GENES CODING FOR
TRIMETHYLAMINE N-OXIDE REDUCTASE, AND USES THEREOF,
ESPECIALLY FOR THE DETECTION OF BACTERIA

<130> 0508-1004

<140> 10/088,117

<141> 2002-03-15

<150> PCT/FR00/02578

<151> 2000-09-15

<150> FR 99/11543

<151> 1999-09-15

<160> 43

<170> PatentIn Ver. 2.1

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gtggctcgga cgctggaagt ctatgaacag cagaccgcct ggccgggtgct ggcggaaaac 660
accgaagtca tgggtgttctg ggccgccgat ccgatcaaga cagcagatat cggctgggtg 720
tatcccgaac atggcgcccta tccggggact gaggcgctca aggccaaggg caccaaggctc 780
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gacctgtatg taaaggactt catcgccaac tacacctcgg gcttcgacaa gttcctgccc 960
tatctgatgg gcgagaccga cagcacgccg aagaccgccg aatgggctgc ggatatcagc 1020
ggcggttcgg ccgagacgat caaggaactg gcgcggctgt tcaaatacga acgcacgatg 1080
ctggcgggcg gctggctgat gcagcggatg catcacggcg agcaggcgca ttggatgctg 1140
gtgacgttgg cctcgatgct gggtcagatc gggctgcggg gcggcggtt cgggctgtcc 1200
tatcactatt cgggcggtgg cagccctcgc agcagcggtc cggcgctttc gggcatcacc 1260
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gtggcgcgcg tggctgacat gctggaaaac cccggcgccg aattcgactt caacggtacg 1380
cggctgaaat tcccggatgt gaagatggcc tattgggttg gcggaacccc ttcgtgtcac 1440
catcaggacc gcaaccgcac ggtcaaggcc tgggaaaaac tggaaacctt catcgtgcat 1500
gacttccagt ggacgcccac ggcgcgccat gccgacatcg tgctgccgcg gacgaccagc 1560
tatgaacgca acgacatcga gacgatcggc gattattcga acaccggcat cctggcgatg 1620
aagaagatcg tcgagccgct ttacgaagcc cgcagcgatt acgacatctt cgccgcggctc 1680
gccgaacggc tgggcaaggg caaggagtgc accgaaggca aggacgagat gggctggatc 1740
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gacgccttct gggcggaagg gatcgtggaa ttcccggta cgcagcgccg ggacttcgtg 1860
cgctatgcc a gcttccggga agatccgctg ctcaacccgc tgggcacgcc gaccggcctg 1920
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acctggatgg aaccgcttga acggctcgac gggccggggg cgaaatatcc gctgcacatc 2040
gcggctcgca cccgttcaac cgggtgactc gcaccgttc accggctcaa cggcacgggtg 2100
ctgcgcgaag gctatgcggg gcaggggac gagccctgcc tgatgcaccc cgacgacgcc 2160
gccgcgcgcg gcatcgccga tggcgacgtg gtgcgggtgc acaatgatcg cggtcagatc 2220
ctgaccgggg tcaaggtgac cgatgcgggt atgaagggg taatccagat ctacgaaggg 2280
ggctggatg atccctcgga cgtgaccgag gcggggacgc tcgacaaata cggcgacgtt 2340
aacgtgctgt cggccgatat cggcatgtcg aaactggcgc agggcaactg tggtcagacc 2400
gtgctggccg aggtcgagaa atacaccggc cccgccgtca ccctgaccgg ctttggctgc 2460
gcgaaggcgg tcgaa 2475

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<210> 8
 <211> 404
 <212> PRT
 <213> Rhodobacter sphaeroides

<400> 8
 Met Gly Arg Ser Cys Gly Gln Ala Ser Glu Ala Lys Val Ile Gly Arg
 1 5 10 15
 Ile Trp Lys Ala Phe Trp Arg Pro Ser Thr Lys Trp Gly Leu Gly Val
 20 25 30
 Leu Leu Val Thr Gly Gly Ile Ala Gly Ala Val Gly Trp Asn Gly Phe
 35 40 45
 His Tyr Val Val Glu Lys Thr Thr Thr Thr Glu Phe Cys Ile Ser Cys
 50 55 60
 His Ser Met Arg Asp Asn Asn Tyr Glu Glu Tyr Lys Thr Thr Ile His
 65 70 75 80

Tyr Gln Asn Thr Ser Gly Val Arg Ala Glu Cys Ala Asp Cys His Val
 85 90 95
 Pro Lys Ser Gly Trp Lys Leu Tyr Arg Ala Lys Leu Leu Ala Ala Lys
 100 105 110
 Asp Leu Trp Gly Glu Ile Arg Gly Thr Ile Asp Thr Arg Glu Lys Phe
 115 120 125
 Glu Ala His Arg Leu Glu Met Ala Glu Thr Val Trp Ala Asp Met Lys
 130 135 140
 Ala Asn Asp Ser Ala Thr Cys Arg Thr Cys His Ser Phe Glu Ala Met
 145 150 155 160
 Asp Phe Ala His Gln Lys Pro Glu Ala Ser Lys Gln Met Gln Gln Ala
 165 170 175
 Met Asn Glu Gly Gly Thr Cys Ile Asp Cys His Lys Gly Ile Ala His
 180 185 190
 Lys Met Pro Asp Met Ala Ser Gly Tyr Arg Ala Leu Phe Ser Lys Leu
 195 200 205
 Glu Lys Ala Ser Gln Ser Leu Lys Pro Arg Lys Gly Glu Thr Leu Tyr
 210 215 220
 Pro Leu Arg Thr Ile Glu Ala Tyr Leu Glu Lys Pro Ser Gly Glu Lys
 225 230 235 240
 Ala Lys Ala Asp Gly Arg Leu Leu Ala Ala Thr Pro Met Gln Val Val
 245 250 255
 Asp Val Thr Gly Asp Trp Val Gln Val Ala Val Lys Gly Trp Gln Gln
 260 265 270
 Glu Gly Ala Glu Arg Val Ile Tyr Glu Lys Gln Gly Lys Arg Ile Phe
 275 280 285
 Asn Ala Ala Leu Ala Pro Ala Ala Thr Gly Ser Val Val Pro Gly Ala
 290 295 300
 Ser Met Val Asp Pro Asp Thr Glu Gln Thr Trp Thr Asp Val Ser Leu
 305 310 315 320
 Thr Ala Trp Val Arg Asn Arg Asp Leu Thr Gly Asp Gln Glu Ala Leu
 325 330 335
 Trp Gln Tyr Gly Lys Gln Met Tyr Asn Gly Ala Cys Gly Met Cys His
 340 345 350
 Val Leu Pro His Pro Glu His Phe Leu Ala Asn Gln Trp Ile Gly Thr
 355 360 365
 Leu Asn Ala Met Lys Ser Arg Ala Pro Leu Asp Asp Glu Gln Phe Arg
 370 375 380

Leu Val Gln Arg Tyr Val Gln Met His Ala Lys Asp Val Glu Pro Glu
 385 390 395 400

Gly Ala Ala Glu

<210> 9
 <211> 2544
 <212> DNA
 <213> Escherichia coli

<400> 9
 atgaacaata acgatctctt tcaggcatca cgtcggcggt ttctggcaca actcggcggc 60
 ttaaccgctc cggggatgct gggggcgtca ttgttaacgc cgcgacgtgc gactgcggcg 120
 caagcggcga ctgacgctgt catctcgaaa gagggcattc ttaccgggtc gactggggg 180
 gctatccgcg cgacgggtgaa ggatgggtcgc tttgtggcgg cgaaaccgtt cgaactggat 240
 aaatatccgt cgaaaatgat tgccggattg ccggatcacg tacacaacgc ggcgcggtatt 300
 cggttatccga tggtagcgtg ggactggctg cgtaagcgcc atctcagcga tacctcccag 360
 cgcggtgata accgttttgt gcgcgtgagc tgggatgaag ccctcgacat gttctatgaa 420
 gaactggaac gcgtgcagaa aactcacggg ccgagtgcct tgctgaccgc cagtgggttg 480
 caatcgacgg ggatgttcca taacgcttcg gggatgcgtg cgaaacgtat tgccttgcat 540
 ggtaatagcg ttggtacggg cggagattac tctaccgggt ctgctgaggt gatcctgccg 600
 cgcgtagtcg gttcgtatgga agtgtatgaa cagcaaacct cctggccgct ggtattgcag 660
 aacagcaaaa ccattgtgct gtggggctcc gatttgctga aaaaccagca agcgaactgg 720
 tgggtgcccg atcacgatgt ttatgaatat tacgcgcagc taaagcgaaa gtcggccgcc 780
 ggtgaaattg aggtcatcag catcgatccg gttgtcacat ccacccatga gtatctgggc 840
 ggggagcatg tgaagcacat tgccgttaac ccgcaaaact acttccttgc taactactgt 960
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 gtgggttttg aggagtctct gccgtatctg ctgggtgaga aagacgggtc gccgaagat 1020
 gccgcattgg gctgaaaaact gagecggcatt gatgccgaaa ccattcgtgg gctggcgcg 1080
 cagatggcgg cgaacagaaac gcaaatattt gctggctggg gcgtgcagcg tatgcagcac 1140
 ggtgaacagt gggcgtggat gattgtgggt ctggcgccga tgctggggca aattggcctg 1200
 ccagggtggg gttttgggtt tggctggcac tacaacggcg caggcacgcc gggcgtaaa 1260
 ggcgttattc tgagtgggtt ctccggctct acgtcgattc cgctgttca cgacaacagt 1320
 gactataaaag gctacagcag cactattccg attgcccgtt ttatcgatgc gatcctcgaa 1380
 ccggggaaaag tgatcaactg gaacggtaaa tcggtaaaaa tgccgccgct gaaaatgtgt 1440
 atttttgccg gaactaacc attccatcgc catcagcaga tcaaccgcgt tattgaaggc 1500
 ttgcgcaacg tggaaaacgg tatcgccata gataaccagt ggacctcaac ctgccgcttt 1560
 gccgatatcg tactgcctgc gaccacgcag tttgagcgta acgatctcga ccagtacggc 1620
 aatcactcca accgtggcat tatcgccatg aaacagggtg tgccgcgcga gttcgaggcg 1680
 cgcaacgact tcgatatttt ccgcgagctg tgccgtcgct ttaatcgca agaagccttt 1740
 accgaagggc tggacgaaat gggctggctg aaacgcattc ggcaggaagg tgtacagcaa 1800
 ggcaaaggac gcggcgttca tctgccagcg tttgatgact tctggaataa caaagagtac 1860
 gtcgagtttg accatccgca gatgtttgtt cgccaccagg cattccgcga agatccggat 1920
 ctcgaaaccg tgggcacgcc gagtggcctg attgagatct actcgaaaac tatcgccgat 1980
 atgaactacg acgattgtca ggggcatccg atgtggtttg agaaaatcga acgctcccac 2040
 ggtgggcctg gctcgcaaaa gtatccgttg catctgcaat ctgtgcatcc ggatttccga 2100
 cttcactcgc agttatgtga gtcggaaacg ctgcgtcacg aatatacggg agcgggtaaa 2160
 gagccagtat tcattaaccc gcaggatgcc agcgcgcgcg gtattcgtaa cggatgatgtg 2220
 gtacgcgtct ttaacgctcg cggtcagggt atggcagggg cagtggtttc tgaccgctat 2280
 gcacccggcg tggcacgaat tcacgaaggg gcatggtagc atccagataa aggcggcgag 2340
 ctgggtgcgc tgtgcaaaata cggtaaaccc aacgtgttga ccacgcacat cggtagatcg 2400
 cagctcgcgc aggtgaccag tgcgcacact acgctgggtg aaattgagaa gtacaacgga 2460
 acagtggagc aggtgacggc gtttaacggc cccgtggaga tgggtggcgca gtgcgaatat 2520
 gttcccgctg cgcaggtgaa atca 2544

<210> 10
 <211> 477
 <212> DNA
 <213> *Salmonella typhimurium*

<400> 10
 atgaaacagg tgggtgtcgcc gcagtttgaa gcgcgtaacg actttgatat tttccgcgat 60
 ctctgccgac gctttaaccg tgaagcggca ttcacggaag gtcttgatga aatgggctgg 120
 ctgaaacgca tctggcagga agggagccag cagggaaaag gtcgcggtat ccacttaccg 180
 attttcgagg tggtctggaa tcaacaggag tacatcgagt ttgatcatcc gcagatgttt 240
 gtacgccatc aggctttccg tgaagatccg gacctggagc cggtgggcac gccaaagcgg 300
 ttgatcgaga tttactccaa aaccatcgcc gacatgcaat acgacgatgg tcagggccat 360
 cccatgtggg tcgaaaaaat cgaacgctcg catggcgggc cgggatcgca gcgctggccg 420
 ctgcacttac aatccgtcca cctgatttc cgtctgcatt cccaactgtt gcgagtc 477

<210> 11
 <211> 390
 <212> PRT
 <213> *Escherichia coli*

<400> 11
 Met Arg Lys Leu Trp Asn Ala Leu Arg Arg Pro Ser Ala Arg Trp Ser
 1 5 10 15
 Val Leu Ala Leu Val Ala Ile Gly Ile Val Ile Gly Ile Ala Leu Ile
 20 25 30
 Val Leu Pro His Val Gly Ile Lys Val Thr Ser Thr Thr Glu Phe Cys
 35 40 45
 Val Ser Cys His Ser Met Gln Pro Val Tyr Glu Glu Tyr Lys Gln Ser
 50 55 60
 Val His Phe Gln Asn Ala Ser Gly Val Arg Ala Glu Cys His Asp Cys
 65 70 75 80
 His Ile Pro Pro Asp Ile Pro Gly Met Val Lys Arg Lys Leu Glu Ala
 85 90 95
 Ser Asn Asp Ile Tyr Gln Thr Phe Ile Ala His Ser Ile Asp Thr Pro
 100 105 110
 Glu Lys Phe Glu Ala Lys Arg Ala Leu Leu Ala Glu Arg Glu Trp Ala
 115 120 125
 Arg Met Lys Glu Asn Asn Ser Ala Thr Cys Arg Ser Cys His Asn Tyr
 130 135 140
 Asp Ala Met Asp His Ala Lys Gln His Pro Glu Ala Ala Arg Gln Met
 145 150 155 160
 Lys Val Ala Ala Lys Asp Asn Gln Ser Cys Ile Asp Cys His Lys Gly
 165 170 175
 Ile Ala His Gln Leu Pro Asp Met Ser Ser Gly Phe Arg Lys Gln Phe
 180 185 190

Asp Asp Val Arg Ala Ser Ala Asn Asp Ser Gly Asp Thr Leu Tyr Ser
 195 200 205
 Ile Asp Ile Lys Pro Ile Tyr Ala Ala Lys Gly Asp Lys Glu Ala Ser
 210 215 220
 Gly Ser Leu Leu Pro Ala Ser Glu Val Lys Val Leu Lys Arg Asp Gly
 225 230 235 240
 Asp Trp Leu Gln Ile Glu Ile Thr Gly Trp Thr Glu Ser Ala Gly Arg
 245 250 255
 Gln Arg Val Leu Thr Gln Phe Pro Gly Lys Arg Ile Phe Val Ala Ser
 260 265 270
 Ile Arg Gly Asp Val Gln Gln Gln Val Lys Thr Leu Glu Lys Thr Thr
 275 280 285
 Val Ala Asp Thr Asn Thr Glu Trp Ser Lys Leu Gln Ala Thr Ala Trp
 290 295 300
 Met Lys Lys Gly Asp Met Val Asn Asp Ile Lys Pro Ile Trp Ala Tyr
 305 310 315 320
 Ala Asp Ser Leu Tyr Asn Gly Thr Cys Asn Gln Cys His Gly Ala Pro
 325 330 335
 Glu Ile Ala His Phe Asp Ala Asn Gly Trp Ile Gly Thr Leu Asn Gly
 340 345 350
 Met Ile Gly Phe Thr Ser Leu Asp Lys Arg Glu Glu Arg Thr Leu Leu
 355 360 365
 Lys Tyr Leu Gln Met Asn Ala Ser Asp Thr Ala Gly Lys Ala His Gly
 370 375 380
 Asp Lys Lys Glu Glu Lys
 385 390

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 12

cggvgaytac tcbachggtg c

21

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 13
 atygatgcga tyctcgaacc 20

<210> 14
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 14
 cgtamwsgtc gakatcgtrr cgctc 25

<210> 15
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 15
 gactcacaya wytgygagtg 20

<210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 16
 tgrccdcgrk cgttaaagac 20

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 17
 ccvggttcga gratcgcac 20

<210> 18
 <211> 16

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 18
 cbgayatcst rctgcc 16

<210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 19
 ggmgaytayt cbacmggygc 20

<210> 20
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 20
 twygarcgya acgaymtcga 20

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 21
 ggvyrcrtacc abscvccttc 20

<210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<220>
 <221> modified_base
 <222> (9)
 <223> a, c, t, g, other or unknown

<400> 22
atcarrccns wvggcgtgcc

20

<210> 23
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 23
gbcacrtcdg tytgygg

17

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<221> modified_base
<222> (3)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (6)
<223> a, c, t, g, other or unknown

<400> 24
acnccngara arttygargc

20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 25
tgyathgayt gycayaargg

20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 26
ccytttrtgrc artcdatrca

20

<210> 27
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<221> modified_base
<222> (3)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (15)
<223> a, c, t, g, other or unknown

<400> 27
ttngcrtcra artgngc

17

<210> 28
<211> 829
<212> PRT
<213> Shewanella c

<400> 28
Met Asn Arg Arg Asp Phe Leu Lys Gly Ile Ala Ser Ser Ser Phe Val
1 5 10 15
Val Leu Gly Gly Ser Ser Val Leu Ala Pro Leu Asn Ala Leu Ala Lys
20 25 30
Thr Gly Ile Asn Glu Asp Glu Trp Leu Thr Thr Gly Ser His Phe Gly
35 40 45
Ala Phe Lys Met Lys Arg Lys Asn Gly Val Ile Ala Glu Val Lys Pro
50 55 60
Phe Asp Leu Asp Lys Tyr Pro Thr Asp Met Ile Asn Gly Ile Arg Asp
65 70 75 80
Met Val Tyr Asn Pro Ser Arg Val Arg Tyr Pro Met Val Arg Leu Asp
85 90 95
Phe Leu Leu Lys Gly His Lys Ser Asn Thr His Gln Arg Gly Asp Phe
100 105 110
Arg Phe Val Arg Val Thr Trp Asp Lys Ala Leu Thr Leu Phe Lys His
115 120 125

Ser Leu Asp Glu Val Gln Thr Gln Tyr Gly Pro Ser Gly Leu His Ala
 130 135 140

Gly Gln Thr Gly Trp Arg Ala Thr Gly Gln Leu His Ser Ser Thr Ser
 145 150 155 160

His Met Gln Arg Ala Val Gly Met His Gly Asn Tyr Val Lys Lys Ile
 165 170 175

Gly Asp Tyr Ser Thr Gly Ala Gly Gln Thr Ile Leu Pro Tyr Val Leu
 180 185 190

Gly Ser Thr Glu Val Tyr Ala Gln Gly Thr Ser Trp Pro Leu Ile Leu
 195 200 205

Glu His Ser Asp Thr Ile Val Leu Trp Ser Asn Asp Pro Tyr Lys Asn
 210 215 220

Leu Gln Val Gly Trp Asn Ala Glu Thr His Glu Ser Phe Ala Tyr Leu
 225 230 235 240

Ala Gln Leu Lys Glu Lys Val Lys Gln Gly Lys Ile Arg Val Ile Ser
 245 250 255

Ile Asp Pro Val Val Thr Lys Thr Gln Ala Tyr Leu Gly Cys Glu Gln
 260 265 270

Leu Tyr Val Asn Pro Gln Thr Asp Val Thr Leu Met Leu Ala Ile Ala
 275 280 285

His Glu Met Ile Ser Lys Lys Leu Tyr Asp Asp Lys Phe Ile Gln Gly
 290 295 300

Tyr Ser Leu Gly Phe Glu Glu Phe Val Pro Tyr Val Met Gly Thr Lys
 305 310 315 320

Asp Gly Val Ala Lys Thr Pro Glu Trp Ala Ala Pro Ile Cys Gly Val
 325 330 335

Glu Ala His Val Ile Arg Asp Leu Ala Lys Thr Leu Val Lys Gly Arg
 340 345 350

Thr Gln Phe Met Met Gly Trp Cys Ile Gln Arg Gln Gln His Gly Glu
 355 360 365

Gln Pro Tyr Trp Met Ala Ala Val Leu Ala Thr Met Ile Gly Gln Ile
 370 375 380

Gly Leu Pro Gly Gly Gly Ile Ser Tyr Gly His His Tyr Ser Ser Ile
 385 390 395 400

Gly Val Pro Ser Ser Gly Ala Ala Ala Pro Gly Ala Phe Pro Arg Asn
 405 410 415

Leu Asp Glu Asn Gln Lys Pro Leu Phe Asp Ser Ser Asp Phe Lys Gly
 420 425 430

Ala Ser Ser Thr Ile Pro Val Ala Arg Trp Ile Asp Ala Ile Leu Glu
 435 440 445
 Pro Gly Lys Thr Ile Asp Ala Asn Gly Ser Lys Val Val Tyr Pro Asp
 450 455 460
 Ile Lys Met Met Ile Phe Ser Gly Asn Asn Pro Trp Asn His His Gln
 465 470 475 480
 Asp Arg Asn Arg Met Lys Gln Ala Phe His Lys Leu Glu Cys Val Val
 485 490 495
 Thr Val Asp Val Asn Trp Thr Ala Thr Cys Arg Phe Ser Asp Ile Val
 500 505 510
 Leu Pro Ala Cys Thr Thr Tyr Glu Arg Asn Asp Ile Asp Val Tyr Gly
 515 520 525
 Ala Tyr Ala Asn Arg Gly Ile Leu Ala Met Gln Lys Met Val Glu Pro
 530 535 540
 Leu Phe Asp Ser Leu Ser Asp Phe Glu Ile Phe Thr Arg Phe Ala Ala
 545 550 555 560
 Val Leu Gly Lys Glu Lys Glu Tyr Thr Arg Asn Met Gly Glu Met Glu
 565 570 575
 Trp Leu Glu Thr Leu Tyr Asn Glu Cys Lys Ala Ala Asn Ala Gly Lys
 580 585 590
 Phe Glu Met Pro Asp Phe Ala Thr Phe Trp Lys Gln Gly Tyr Val His
 595 600 605
 Phe Gly Asp Gly Glu Leu Trp Thr Arg His Ala Asp Phe Arg Asn Asp
 610 615 620
 Pro Glu Ile Asn Pro Leu Gly Thr Pro Ser Gly Leu Ile Glu Ile Phe
 625 630 635 640
 Ser Arg Lys Ile Asp Gln Phe Gly Tyr Asp Asp Cys Lys Gly His Pro
 645 650 655
 Thr Trp Met Glu Lys Thr Glu Arg Ser His Gly Gly Pro Gly Ser Asp
 660 665 670
 Lys His Pro Ile Trp Leu Gln Ser Cys His Pro Asp Lys Arg Leu His
 675 680 685
 Ser Gln Met Cys Glu Ser Arg Glu Tyr Arg Glu Thr Tyr Ala Val Asn
 690 695 700
 Gly Arg Glu Pro Val Tyr Ile Ser Pro Val Asp Ala Lys Ala Arg Gly
 705 710 715 720
 Ile Lys Asp Gly Asp Ile Val Arg Val Phe Asn Asp Arg Gly Gln Leu
 725 730 735

Leu Ala Gly Ala Val Val Ser Asp Asn Phe Pro Thr Gly Ile Val Arg
 740 745 750

Ile His Glu Gly Ala Trp Tyr Gly Pro Val Gly Lys Asp Gly Ser Thr
 755 760 765

Glu Gly Gly Ala Glu Val Gly Ala Leu Cys Ser Tyr Gly Asp Pro Asn
 770 775 780

Thr Leu Thr Leu Asp Ile Gly Thr Ser Lys Leu Ala Gln Ala Cys Ser
 785 790 795 800

Ala Tyr Thr Cys Leu Val Glu Phe Glu Lys Tyr Gln Gly Lys Val Pro
 805 810 815

Lys Val Ser Ser Phe Asp Gly Pro Ile Glu Val Glu Ile
 820 825

<210> 29

<211> 244

<212> PRT

<213> Photobacterium phosphoreum

<400> 29

Thr Ile Leu Lys Asp Cys Lys Thr Leu Ile Trp Trp Ser Asn Asp Pro
 1 5 10 15

Ile Lys Asn Ser Gln Val Gly Trp Gln Cys Glu Thr His Gly Ser Tyr
 20 25 30

Glu Tyr Tyr Ala Gln Leu Lys Gln Lys Val Ala Asp Gly Gly Ile Arg
 35 40 45

Met Ile Ser Val Asp Pro Val Val Ser Lys Ser Gln Lys Tyr Phe Asn
 50 55 60

Cys Glu His Gln Tyr Val Asn Pro Gln Thr Asp Val Pro Phe Met Leu
 65 70 75 80

Ala Ile Ala His Thr Leu Tyr Lys Glu Asp Leu Tyr Asp Lys Gln Phe
 85 90 95

Leu Glu Thr Tyr Thr Leu Gly Phe Asn Glu Phe Leu Pro Tyr Leu Leu
 100 105 110

Gly Thr Gly Lys Asp Lys Ile Ala Lys Thr Pro Glu Trp Ala Glu Pro
 115 120 125

Ile Cys Gly Val Lys Ala Glu Ala Ile Arg Glu Phe Ala Arg Gly Leu
 130 135 140

Val Lys Asn Arg Thr Met Ile Met Phe Gly Trp Ala Val Gln Arg Gln
 145 150 155 160

Gln His Gly Glu Gln Pro Tyr Trp Met Gly Ala Val Leu Ala Ser Met
 165 170 175

Leu Gly Gln Ile Gly Leu Pro Gly Gly Gly Ile Ser Tyr Ser His Phe
 180 185 190

Tyr Ser Gly Val Gly Leu Pro Phe Ser Thr Ala Ala Gly Pro Gly Gly
 195 200 205

Phe Pro Arg Asn Val Asp Glu Gly Gln Gln Pro Ile Trp Asn Asn Asn
 210 215 220

Asp Leu Lys Ala Thr Val Arg Gln Phe Arg Ser Gln Asp Gly Leu Met
 225 230 235 240

Arg Ser Ser Asn

<210> 30

<211> 257

<212> PRT

<213> Shewanella massilia

<400> 30

Gly Thr Ser Trp Pro Leu Ile Leu Glu His Ser Asp Thr Ile Val Leu
 1 5 10 15

Trp Ser Asn Asp Pro Tyr Lys Asn Leu Gln Val Gly Trp Asn Ala Glu
 20 25 30

Thr His Glu Ser Phe Ala Tyr Leu Ala Gln Leu Lys Glu Lys Val Lys
 35 40 45

Gln Gly Lys Ile Arg Val Ile Ser Ile Asp Pro Val Val Thr Lys Thr
 50 55 60

Gln Ala Tyr Leu Gly Cys Glu Gln Leu Tyr Val Asn Pro Gln Thr Asp
 65 70 75 80

Val Thr Leu Met Leu Ala Ile Ala His Glu Met Ile Ser Lys Lys Leu
 85 90 95

Tyr Asp Asp Lys Phe Ile Gln Gly Tyr Ser Leu Gly Phe Glu Glu Phe
 100 105 110

Val Pro Tyr Val Met Gly Thr Lys Asp Gly Val Ala Lys Thr Pro Glu
 115 120 125

Trp Ala Ala Pro Ile Cys Gly Val Glu Ala His Val Ile Arg Asp Leu
 130 135 140

Ala Lys Thr Leu Val Lys Gly Arg Thr Gln Phe Met Met Gly Trp Cys
 145 150 155 160

Ile Gln Arg Gln Gln His Gly Glu Gln Pro Tyr Trp Met Pro Ala Val
 165 170 175

Leu Ala Thr Met Ile Gly Gln Ile Gly Leu Pro Gly Gly Glu Ile Ser
 180 185 190

Tyr Gly His His Tyr Ser Ser Ile Gly Val Pro Ser Ser Gly Ala Ala
 195 200 205

Ala Pro Gly Ala Phe Pro Arg Asn Leu Asp Glu Asn Gln Lys Pro Leu
 210 215 220

Phe Asp Ser Ser Asp Phe Lys Gly Ala Ser Ser Thr Ile Pro Val Ala
 225 230 235 240

Arg Trp Ile Asp Ala Ile Leu Glu Pro Gly Lys Thr Ile Asp Ala Asn
 245 250 255

Gly

<210> 31
 <211> 258
 <212> PRT
 <213> Escherichia coli

<400> 31
 Gln Thr Ser Trp Pro Leu Val Leu Gln Asn Ser Lys Thr Ile Val Leu
 1 5 10 15

Trp Gly Ser Asp Leu Leu Lys Asn Gln Gln Ala Asn Trp Trp Cys Pro
 20 25 30

Asp His Asp Val Tyr Glu Tyr Tyr Ala Gln Leu Lys Arg Lys Ser Ala
 35 40 45

Ala Gly Glu Ile Glu Val Ile Ser Ile Asp Pro Val Val Thr Ser Thr
 50 55 60

His Glu Tyr Leu Gly Gly Glu His Val Lys His Ile Ala Val Asn Pro
 65 70 75 80

Gln Thr Asp Val Pro Leu Gln Leu Ala Leu Ala His Thr Leu Tyr Ser
 85 90 95

Glu Asn Leu Tyr Asp Lys Asn Phe Leu Ala Asn Tyr Cys Val Gly Phe
 100 105 110

Glu Glu Phe Leu Pro Tyr Leu Leu Gly Glu Lys Asp Gly Gln Pro Lys
 115 120 125

Asp Ala Ala Trp Ala Glu Lys Leu Ser Gly Ile Asp Ala Glu Thr Ile
 130 135 140

Arg Gly Leu Ala Arg Gln Met Ala Ala Asn Arg Thr Gln Ile Ile Ala
 145 150 155 160

Gly Trp Cys Val Gln Arg Met Gln His Gly Glu Gln Trp Ala Trp Met
 165 170 175

Ile Val Val Leu Ala Ala Met Leu Gly Gln Ile Gly Leu Pro Gly Gly
 180 185 190

Gly Phe Gly Phe Gly Trp His Tyr Asn Gly Ala Gly Thr Pro Gly Arg
 195 200 205
 Lys Gly Val Ile Leu Ser Gly Phe Ser Gly Ser Thr Ser Ile Pro Pro
 210 215 220
 Val His Asp Asn Ser Asp Tyr Lys Gly Tyr Ser Ser Thr Ile Pro Ile
 225 230 235 240
 Ala Arg Phe Ile Asp Ala Ile Leu Glu Pro Gly Lys Val Ile Asn Trp
 245 250 255

Asn Gly

<210> 32
 <211> 250
 <212> PRT
 <213> Rhodobacter sphaeroides

<400> 32
 Gln Thr Ala Trp Pro Val Val Val Glu Asn Thr Asp Leu Met Val Phe
 1 5 10 15
 Trp Ala Ala Asp Pro Met Lys Thr Asn Glu Ile Gly Trp Val Ile Pro
 20 25 30
 Asp His Gly Ala Tyr Ala Gly Met Lys Ala Leu Lys Glu Lys Gly Thr
 35 40 45
 Arg Val Ile Cys Ile Asn Pro Val Arg Thr Glu Thr Ala Asp Tyr Phe
 50 55 60
 Gly Ala Asp Val Val Ser Pro Arg Pro Gln Thr Asp Val Ala Leu Met
 65 70 75 80
 Leu Gly Met Ala His Thr Leu Tyr Ser Glu Asp Leu His Asp Lys Asp
 85 90 95
 Phe Leu Glu Asn Cys Thr Thr Gly Phe Asp Leu Phe Ala Ala Tyr Leu
 100 105 110
 Thr Gly Glu Ser Asp Gly Thr Pro Lys Thr Ala Glu Trp Ala Ala Glu
 115 120 125
 Ile Cys Gly Leu Pro Ala Glu Gln Ile Arg Glu Leu Ala Arg Ser Phe
 130 135 140
 Val Ala Gly Arg Thr Met Leu Ala Ala Gly Trp Ser Ile Gln Arg Met
 145 150 155 160
 His His Gly Glu Gln Ala His Trp Met Leu Val Thr Leu Ala Ser Met
 165 170 175
 Ile Gly Gln Ile Gly Leu Pro Gly Gly Gly Phe Gly Leu Ser Tyr His
 180 185 190

Tyr Ser Asn Gly Gly Ser Pro Thr Ser Asp Gly Pro Ala Leu Gly Gly
 195 200 205
 Ile Ser Asp Gly Gly Lys Ala Val Glu Gly Ala Ala Trp Leu Ser Glu
 210 215 220
 Ser Gly Ala Thr Ser Ile Pro Cys Ala Arg Val Val Asp Met Leu Leu
 225 230 235 240
 Asn Pro Gly Gly Glu Phe Gln Phe Asn Gly
 245 250

<210> 33
 <211> 37
 <212> DNA
 <213> *Shewanella massilia*

<400> 33
 aaaatcggcg actactccac aggtgcaggc caaacta

37

<210> 34
 <211> 37
 <212> DNA
 <213> *Shewanella putrefaciens*

<400> 34
 aaaatcggcg actactccac cggtgcaggc caaacca

37

<210> 35
 <211> 37
 <212> DNA
 <213> *Shewanella c*

<400> 35
 aaaatcggcg actactccac aggtgcaggc caaacaa

37

<210> 36
 <211> 37
 <212> DNA
 <213> *Escherichia coli*

<400> 36
 acgggcggag attactctac cggtgctgag caggtga

37

<210> 37
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
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<400> 37
cggcgactac tctacaggtg c

21

<210> 38
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 38
cggvgaytac tcbachggtg c

21

<210> 39
<211> 37
<212> DNA
<213> Escherichia coli

<400> 39
acgggaggag attactctac cggcgcaggc caaacca

37

<210> 40
<211> 37
<212> DNA
<213> Rhodobacter sphaeroides

<400> 40
tcgtcgggag actattcgac cggcgcaggc caaacaa

37

<210> 41
<211> 37
<212> DNA
<213> Rhodobacter capsulatus

<400> 41
ggcgcgggag attattcgac cggcgcaggc cagggtga

37

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 42
ggcgactatt ctacaggcgc

20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 43
ggmgaytayt cbacmggygc